



## SEQUENCE LISTING

<110> Duvick, Jonathan P.  
Gilliam, Jacob T.  
Maddox, Joyce R.  
Rao, Aragula Gururaj  
Crasta, Oswald R.  
Folkerts, Otto

<120> Amino Polyol Amine Oxidase  
Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134R

<150> US 60/092,936

<151> 1998-07-25

<150> US 60/135,391

<151> 1999-05-21

<150> US 09/352,159

<151> 1999-07-12

<150> US 09/352,168

<151> 1999-07-12

<160> 53

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> *Exophiala spinifera*

<220>

<221> misc\_feature

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attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtea cagctcgatt	180
ggaggacgac cgagaagcct tgttcgcgac accacggctt gtcccatacg aagactatct	240
tgctatagta gccacggata gaattttccg caaatgcttg cttctcggcg ggaagaggtg	300
gtgaaaatgt caaggtggga tacaaggttg tggtaacga aaccancacc ttttgcttc	360
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<210> 2

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<213> *Exophiala spinifera*

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gacgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc	180
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 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 3	
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<210> 4  
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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt	96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	

ccc ggc agc acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
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Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp		
				85					90						95		
ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	336	
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu		
			100					105					110				
ggt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	384	
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile		
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gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gag	aag	egg	432	
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg		
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ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	480	
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu		
145					150					155					160		
cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	528	
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly		
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gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	576	
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys		
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agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	624	
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly		
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cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	672	
Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met		
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Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala		
225					230					235					240		
gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	768	
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly		
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gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	816	
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu		
			260					265					270				
tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	864	
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala		
		275					280					285					
ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	912	
Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val		
	290					295				300							
tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	960	
Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln		
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tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc	1008
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
325 330 335	
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	
340 345 350	
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac	1104
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp	
355 360 365	
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
370 375 380	
gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa gga	1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	
385 390 395 400	
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgg	1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser	
405 410 415	
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg	1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr	
420 425 430	
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt caa	1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln	
435 440 445	
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	1386
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
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tag	1389

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 <212> PRT  
 <213> *Exophiala spinifera*

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35 40 45	
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
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Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
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<221> CDS

<222> (700)...(1439)

<400> 7

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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt	96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggg aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcc gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgctcgtctca ggtgggggac	676
Gln Tyr Val Arg Cys Lys Thr	

210	215	
tcgtttctca gtgggtcattc cag gt atg cag tcg att tgc cat gcc atg tca		728
	Gly Met Gln Ser Ile Cys His Ala Met Ser	
	220 225	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa		776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu		
	230 235 240	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc		824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala		
	245 250 255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat		872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr		
	260 265 270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg		920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu		
	275 280 285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg		968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp		
	290 295 300 305	
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Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser		
	310 315 320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat		1064
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp		
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cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag		1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys		
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tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa		1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln		
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ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc		1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala		
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aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct		1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala		
	390 395 400	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg		1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala		
	405 410 415	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag aag tct		1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser		
	420 425 430	

tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt caa cga 1400  
 Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg  
 435 440 445

ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1442  
 Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 450 455 460

<210> 8  
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 <212> PRT  
 <213> *Exophiala spinifera*

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 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
 35 40 45  
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
 50 55 60  
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
 65 70 75 80  
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
 85 90 95  
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
 100 105 110  
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
 115 120 125  
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
 130 135 140  
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
 145 150 155 160  
 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
 165 170 175  
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
 180 185 190  
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
 195 200 205  
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
 210 215 220  
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
 225 230 235 240  
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
 245 250 255  
 Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu  
 260 265 270  
 Tyr Pro Thr Leu Thr Phe Ser Pro Leu Pro Ala Glu Lys Gln Ala  
 275 280 285  
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
 290 295 300  
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
 305 310 315 320  
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
 325 330 335  
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg



			340					345					350				
Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp		
		355					360					365					
Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro		
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385					390					395				400			
Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser		
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Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr		
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Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln		
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<211> 458

<212> PRT

<213> *Exophiala spinifera*

<400> 9

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Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly		
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Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp		
	50					55					60						
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu		
65				70						75				80			
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp		
			85					90					95				
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu		
			100					105					110				
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile		
		115					120					125					
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg		
	130					135					140						
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu		
145					150					155				160			
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly		
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Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys		
		180						185					190				
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly		
	195					200						205					
Gln	Tyr	Val	Arg	Cys	Lys	Thr	Gly	Ala	Cys	Gly	Val	Val	Ser	Gly	Gly		
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Gly	Leu	Val	Ser	Gln	Trp	Ser	Phe	Gln	Val	Cys	Ser	Arg	Phe	Ala	Met		
225					230					235				240			
Pro	Cys	Gln	Arg	Asn	Leu	Phe	Gln	Ala	Gln	Cys	Thr	Ser	Thr	Pro	Pro		
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Ser	Leu	Lys	Leu	Ser	Ser	Arg	His	Pro	Ala	Val	Gln	Tyr	Asp	Arg	Pro		
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Arg	Ala	Pro	Cys	Ser	Glu	Ala	Lys	Arg	Trp	Trp	Phe	Arg	Tyr	Arg	Gln		
	275						280						285				

Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys  
 290 295 300  
 His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr  
 305 310 315 320  
 Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn  
 325 330 335  
 Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser  
 340 345 350  
 Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly  
 355 360 365  
 Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr  
 370 375 380  
 Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg  
 385 390 395 400  
 Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu  
 405 410 415  
 Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg  
 420 425 430  
 Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu  
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<210> 10  
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 <213> *Exophiala spinifera*

<220>  
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 <222> (1)...(1389)  
 <221> misc\_feature  
 <222> (1)...(3)  
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 ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 20 25 30  
 ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgc 144  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45  
 ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 50 55 60  
 gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 65 70 75 80  
 gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	

305	310	315	320	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac				1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp				
325		330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga				1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly				
340		345	350	
egg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg				1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp				
355		360	365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag				1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu				
370		375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tcc aag cag cag tat ttc caa				1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln				
385		390	400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt				1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly				
405		410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag				1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu				
420		425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcc ggt				1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly				
435		440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca				1389
Gln Arg Gly Ala Ala Glu Val Ala Ser Leu Val Pro Ala Ala				
450		455	460	
tag				1392

<210> 11  
 <211> 463  
 <212> PRT  
 <213> *Exophiala spinifera*

<400> 11  
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 1 5 10 15  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 20 25 30  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 50 55 60  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 65 70 75 80  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 85 90 95



ggggaattca aagacaacgt tgcggacgtg gtag 34

<210> 13  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer sequence designed for cloning DNA into  
 expression vectors, N23259

<400> 13  
 ggggcggcgc cctatgctgc tggcaccagg ctag 34

<210> 14  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 14  
 tggtttcggt accgacaacc ttgtatccc 29

<210> 15  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide for 5' race, N21968

<400> 15  
 gagttggtcc cagacagact tttgtcgt 28

<210> 16  
 <211> 1673  
 <212> DNA  
 <213> *Exophiala spinifera*

<220>  
 <221> sig\_peptide  
 <222> (1)...(267)  
 <223> yeast alpha mating factor secretion signal.

<221> CDS  
 <222> (1)...(1662)

<400> 16  
 atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc 48  
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser  
 -85 -80 -75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96  
 Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln  
 -70 -65 -60

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe -55 -50 -45	144
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu -40 -35 -30	192
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val -25 -20 -15 -10	240
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala -5 1 5	288
gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg 10 15 20	336
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp 25 30 35	384
cgt gta ggg gga aag act ctg agc gta caa tgc ggt ccc ggc agg acg Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr 40 45 50 55	432
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser 60 65 70	480
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln 75 80 85	528
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr 90 95 100	576
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala 105 110 115	624
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser 120 125 130 135	672
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val 140 145 150	720
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu 155 160 165	768
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac	816

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His	
170 175 180	
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt	864
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly	
185 190 195	
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga	912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg	
200 205 210 215	
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt	960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu	
220 225 230	
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag	1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln	
235 240 245	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga	1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg	
250 255 260	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg	1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu	
265 270 275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat	1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn	
280 285 290 295	
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg	1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro	
300 305 310	
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac	1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp	
315 320 325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg	1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp	
330 335 340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa	1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln	
345 350 355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc ccg gca	1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala	
360 365 370 375	
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc	1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu	
380 385 390	
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc	1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala	
395 400 405	



gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgc gcg ctc aga acg	1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr	
410 415 420	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg	1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp	
425 430 435	
aaa ggg tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca	1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala	
440 445 450 455	
gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c	1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala	
460 465	

<210> 17  
 <211> 554  
 <212> PRT  
 <213> *Exophiala spinifera*

<220>  
 <221> SIGNAL  
 <222> (1)...(89)

<400> 17	
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Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln	
-70 -65 -60	
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe	
-55 -50 -45	
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu	
-40 -35 -30	
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val	
-25 -20 -15 -10	
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala	
-5 1 5	
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg	
10 15 20	
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp	
25 30 35	
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr	
40 45 50 55	
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser	
60 65 70	
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln	
75 80 85	
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr	
90 95 100	
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala	
105 110 115	
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser	
120 125 130 135	
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val	
140 145 150	

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu  
 155 160 165  
 Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His  
 170 175 180  
 Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly  
 185 190 195  
 Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg  
 200 205 210 215  
 Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu  
 220 225 230  
 Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln  
 235 240 245  
 Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg  
 250 255 260  
 Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu  
 265 270 275  
 Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn  
 280 285 290 295  
 Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro  
 300 305 310  
 Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp  
 315 320 325  
 Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp  
 330 335 340  
 Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln  
 345 350 355  
 Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala  
 360 365 370 375  
 Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu  
 380 385 390  
 Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala  
 395 400 405  
 Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr  
 410 415 420  
 Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp  
 425 430 435  
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala  
 440 445 450 455  
 Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 460 465

<210> 18  
 <211> 2079  
 <212> DNA  
 <213> Unknown

<220>

<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1  
 - 687, gst fusion + polylinker, 688-2076,  
 K:trAPAO, extra lysine underlined; 2077-2079, stop  
 codon. For bacterial expression.

<221> CDS  
 <222> (1)...(2076)  
 <221> misc\_feature  
 <222> (1)...(687)

<223> gst fusion + polylinker

<221> misc\_feature

<222> (688)...(2076)

<223> K:trAPAO

<221> misc\_feature

<222> (688)...(690)

<223> Extra lysine

<400> 18

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggt gat cat gla acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc	720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly	
225 230 235 240	
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt	768
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	
245 250 255	
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act	816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	
260 265 270	
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc	864
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly	
275 280 285	
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt	912
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe	
290 295 300	
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca	960
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser	
305 310 315 320	
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac	1008
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp	
325 330 335	
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc	1056
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro	
340 345 350	
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg	1104
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala	
355 360 365	
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt	1152
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys	
370 375 380	
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc	1200
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile	
385 390 395 400	
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt	1248
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe	
405 410 415	
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg	1296

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	
420 425 430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag	1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	
435 440 445	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac	1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
450 455 460	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca	1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
465 470 475 480	
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
485 490 495	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
500 505 510	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	
515 520 525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc	1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly	
530 535 540	
ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga	1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	
545 550 555 560	
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg	1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	
565 570 575	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga	1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	
580 585 590	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg	1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly	
595 600 605	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag	1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys	
610 615 620	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat	1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp	
625 630 635 640	
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat	1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His	
645 650 655	

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg	2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly	
660 665 670	

gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg	2064
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675 680 685	

gtg cca gca gca tag	2079
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690	

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Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
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Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
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Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
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Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
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Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
			100					105					110				
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
		115					120					125					
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
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Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
145					150					155				160			
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
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Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180					185					190				
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195					200					205					
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
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Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly		
225					230					235					240		
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly		
				245					250					255			
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr		
			260					265					270				
Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly		
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Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe		
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Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	305	310	315	320
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	325	330	335	
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	340	345	350	
Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	355	360	365	
Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	370	375	380	
Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	385	390	395	400
Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	405	410	415	
Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	420	425	430	
Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	435	440	445	
Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	450	455	460	
Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	465	470	475	480
Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	485	490	495	
Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	500	505	510	
Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	515	520	525	
Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	530	535	540	
Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	545	550	555	560
Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	565	570	575	
Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	580	585	590	
Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	595	600	605	
Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	610	615	620	
Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	625	630	635	640
Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	645	650	655	
Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	660	665	670	
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<212> DNA

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<220>

<223> Nucleotide sequence of K:trAPAO translational

fusion with barley alpha amylase signal sequence,  
for expression and secretion of the mature trAPAO  
in maize. Nucleotides 1-72, barley alpha amylase  
signal sequence, nucleotides 73-75, added lysine  
residue; nucleotides 76 -1464 , trAPAO cDNA.

<221> sig\_peptide  
<222> (1)...(72)  
<223> Barley alpha amylase signal sequence

<221> misc\_feature  
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ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta      96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
          -5                      1                      5

gtg gtg ggc gct gcc ttg agc ggt ttg gag acg gca cgc aaa gtc cag      144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
          10                      15                      20

gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg      192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
          25                      30                      35                      40

gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac      240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
          45                      50                      55

gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc      288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
          60                      65                      70

aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act      336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
          75                      80                      85

gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct      384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
          90                      95                      100

tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa      432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
          105                      110                      115                      120

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125 130 135	
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Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala	
140 145 150	
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca	576
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala	
155 160 165	
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc	624
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser	
170 175 180	
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat	672
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn	
185 190 195 200	
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca	720
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr	
205 210 215	
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc	768
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly	
220 225 230	
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc	816
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser	
235 240 245	
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Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys	
250 255 260	
gtg gtg gtc tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca	912
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser	
265 270 275 280	
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg	960
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu	
285 290 295	
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc	1008
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg	
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315 320 325	
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Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr	
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[illegible]

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Leu Leu Pro Val Trp	Ser Gln Leu Ile Glu	Glu His Ser Leu Gln Asp		
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Leu Lys Ala Ser Pro	Gln Ala Lys Arg	Leu Asp Ser Val Ser Phe Ala		
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His Tyr Cys Glu Lys	Glu Leu Asn Leu Pro	Ala Val Leu Gly Val Ala		
	155		160	165
Asn Gln Ile Thr Arg	Ala Leu Leu Gly Val	Glu Ala His Glu Ile Ser		
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Met Leu Phe Leu Thr	Asp Tyr Ile Lys Ser	Ala Thr Gly Leu Ser Asn		
185		190		200
Ile Phe Ser Asp Lys	Lys Asp Gly Gly Gln	Tyr Met Arg Cys Lys Thr		
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Gly Met Gln Ser Ile	Cys His Ala Met Ser	Lys Glu Leu Val Pro Gly		
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Ser Val His Leu Asn	Thr Pro Val Ala Glu	Ile Glu Gln Ser Ala Ser		
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Gly Cys Thr Val Arg	Ser Ala Ser Gly Ala	Val Phe Arg Ser Lys Lys		
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Val Val Val Ser Leu	Pro Thr Thr Leu Tyr	Pro Thr Leu Thr Phe Ser		
265		270		275
Pro Pro Leu Pro Ala	Glu Lys Gln Ala Leu	Ala Glu Asn Ser Ile Leu		
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Gly Tyr Tyr Ser Lys	Ile Val Phe Val Trp	Asp Lys Pro Trp Trp Arg		
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Glu Gln Gly Phe Ser	Gly Val Leu Gln Ser	Ser Cys Asp Pro Ile Ser		
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Phe Ala Arg Asp Thr	Ser Ile Asp Val Asp	Arg Gln Trp Ser Ile Thr		
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Cys Phe Met Val Gly	Asp Pro Gly Arg Lys	Trp Ser Gln Gln Ser Lys		
345		350		355
Gln Val Arg Gln Lys	Ser Val Trp Asp Gln	Leu Arg Ala Ala Tyr Glu		
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Asn Ala Gly Ala Gln	Val Pro Glu Pro Ala	Asn Val Leu Glu Ile Glu		
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Trp Ser Lys Gln Gln	Tyr Phe Gln Gly Ala	Pro Ser Ala Val Tyr Gly		
	395		400	405
Leu Asn Asp Leu Ile	Thr Leu Gly Ser Ala	Leu Arg Thr Pro Phe Lys		
	410		415	420
Ser Val His Phe Val	Gly Thr Glu Thr Ser	Leu Val Trp Lys Gly Tyr		
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Met Glu Gly Ala Ile	Arg Ser Gly Gln Arg	Gly Ala Ala Glu Val Val		
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gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg	96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115 120 125	
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg	432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
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gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
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cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165 170 175	
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Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
180 185 190	
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta	624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val	
195 200 205	
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg	672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	
210 215 220	
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct	720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala	

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gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260 265 270				816
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275 280 285				864
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aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340 345 350				1056
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aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405 410 415				1248
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420 425 430				1296
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 435 440 445				1344
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460				1392

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Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465 470 475 480	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
485 490 495	
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Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
500 505 510	
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515 520 525	
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Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530 535 540	
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Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
545 550 555 560	
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Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
565 570 575	
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Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
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595 600	

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<213> *Exophiala spinifera*

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35 40 45	
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	



Val Ala Ser Leu Val Pro Ala Ala  
580 585 590  
595 600

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<212> DNA  
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espl mat: an artificial spacer sequence and  
K:trAPAO

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<221> CDS  
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Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr  
45 50 55



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Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	
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Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	
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Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	
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Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg	
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Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile	
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Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr	
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Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly	
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ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tgc gca	2352

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Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile		
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Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile		
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Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile		
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Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser		
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gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	gaa	atc	2784	
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile		
	890					895						900					
gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	gtc	tat	2832	
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr		
905					910					915					920		
ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggt	tcg	gcg	ctc	aga	acg	ccg	ttc	2880	
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe		
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Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly		
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Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val		
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Arg	Glu	Ile	Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Ser	Ala	Gly
	75						80					85			
Glu	Ser	Glu	Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu
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Asn	Thr	Asn	Lys	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu	Glu
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Tyr	Gly	Trp	Asn	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala	Ala
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Asn	Gln	Asp	Val	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile	Leu
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Gly	Phe	Pro	Ala	Ala	Pro	Gln	Leu	Pro	Ile	Thr	Gln	Arg	Asn	Leu	Gly
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Phe	Leu	Asp	Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala
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Ala	Phe	Gly	Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala
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Gly	Gly	Arg	Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro
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Pro	Phe	Arg	Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe
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Ile Ala Ala Ile	Glu Thr Glu Val Arg Phe	Gln Cys Pro Ser Ala Ile		
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Val Ala Gln Asp	Ser Arg Asn Arg Gly Ile	Pro Ser Trp Arg Tyr Tyr		
	380	385	390	
Tyr Asn Ala Thr	Phe Glu Asn Leu Glu Leu Phe	Pro Gly Ser Glu Val		
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Tyr His Ser Ser	Glu Val Gly Met Val Phe Gly Thr	Tyr Pro Val Ala		
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Trp Ala Ala Phe	Ala Lys Asn Pro Met Asn Gly	Pro Gly Trp Lys Gln		
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Asp Val Ser Pro	Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg			
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Tyr Tyr Thr Glu	Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly			
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Val Val Val Gly	Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
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Gln Ala Ala Gly	Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val			
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Gly Gly Lys Thr	Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile			
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Asn Asp Leu Gly	Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val			
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Thr Gly Asn Ser	Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala			
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Pro Tyr Gly Asp	Ser Leu Leu Ser Glu Val Ala Ser Ala Leu Ala			
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Glu Leu Leu Pro	Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln			
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Asp Leu Lys Ala	Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe			
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Ala His Tyr Cys	Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			
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Ala Asn Gln Ile	Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			
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Ser Met Leu Phe	Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			
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Asn Ile Phe Ser	Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			
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Thr Gly Met Gln	Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			
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Gly Ser Val His	Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
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Ser Gly Cys Thr	Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
	765	770	775	
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Ser Pro Pro Leu	Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			



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Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	
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Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	
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Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg	
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Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu	
185 190 195 200	



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Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro	
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Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp	
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Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu	
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Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn	
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Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val	
395 400 405	
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Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro	
410 415 420	
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc	1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val	

425	430	435	440	
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct				1410
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro				
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gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc				1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg				
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Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly				
	475	480	485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc				1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser				
	490	495	500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt				1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly				
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ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt				1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val				
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ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg				1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser				
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Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn				
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gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg				1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu				
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gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa				1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln				
	585	590	595	600
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag				1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu				
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gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg				1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu				
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atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag				2016
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys				
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Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn				
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caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 825 830 835 840	2592
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cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 860 865 870	2688
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 875 880 885	2736
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 890 895 900	2784

890	895	900	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
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tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
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acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
	940	945	950
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca			2973
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Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg			
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Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe			
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Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala			
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Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser			
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Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly			
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Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala			
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Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn			
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Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr			
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Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg			
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Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val			
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Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu			
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Pro	Gln	Thr	Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	
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Phe	Lys	Leu	Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	
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 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
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 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
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 bacterial expression.

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Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro	
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Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro	
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gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac	1200
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385 390 395 400	



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ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala 580 585 590	1776
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595 600 605	1824
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala 610 615 620	1872
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc	1920

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Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr	
645 650 655	
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc	2016
Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala	
660 665 670	
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat	2064
Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn	
675 680 685	
gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct	2112
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Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr	
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Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly	
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Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val	
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Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala	
755 760 765	
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Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys	
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Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu	
785 790 795 800	
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Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu	
805 810 815	
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Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn	
820 825 830	
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt	2544
Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly	
835 840 845	
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc	2592
Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu	
850 855 860	

ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag	2640
Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys	
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gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac	2688
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr	
885 890 895	
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Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln	
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atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt	2784
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu	
915 920 925	
ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc	2832
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe	
930 935 940	
tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg	2880
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met	
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cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg	2928
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val	
965 970 975	
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt	2976
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys	
980 985 990	
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg	3024
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val	
995 1000 1005	
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct	3072
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro	
1010 1015 1020	
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac	3120
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr	
1025 1030 1035 1040	
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa	3168
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln	
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ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc	3216
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala	
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aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc	3264
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe	
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cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc	3360
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ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg	3408
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser	
	1125 1130 1135
aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac	3456
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn	
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gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt	3504
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val	
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cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa	3552
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu	
	1170 1175 1180
ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc	3600
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Leu Val Pro Ala Ala	
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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
	35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
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Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
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Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
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Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
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Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
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Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu	Val	Tyr	His	Ser	625	630	635	640
Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala	Ser	Ala	Thr	645	650	655	
Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly	Ala	Trp	Ala	Ala	660	665	670	
Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys	Gln	Val	Pro	Asn	675	680	685	
Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln	Val	Asp	Val	Ser	690	695	700	
Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Arg	Tyr	Tyr	Thr	705	710	715	720
Glu	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Ser	Gly	Gly	725	730	735	
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Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	770	775	780	
Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	785	790	795	800
Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	805	810	815	
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Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	835	840	845	
Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	850	855	860	
Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	865	870	875	880
Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	885	890	895	
Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	900	905	910	
Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	915	920	925	
Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	930	935	940	
Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	945	950	955	960
Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	965	970	975	
His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	980	985	990	
Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	995	1000	1005	
Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	1010	1015	1020	
Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	1025	1030	1035	1040
Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	1045	1050	1055	
Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	1060	1065	1070	
Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	1075	1080	1085	

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 Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala  
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 1125 1130 1135  
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 His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu  
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 bacterial expression vector pGEX-4T-1 or similar  
 vector. gst:BST1:sp:K:trAPAO fusion, 3591 nt.  
 1-687 gst  
 + polylinker, 688-2163, BEST1 mature; 2164-2199,  
 spacer, 2200-3588, K:trAPAO

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48

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tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
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Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
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gga gcg gtt ttg gat att aga tac ggt gtt tgc aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
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ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
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Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
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Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
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Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
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Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly	
225 230 235 240	
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Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His	
260 265 270	
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Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp	
275 280 285	
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Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val	
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Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala	
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Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg	
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Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro	
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Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu	
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Thr Arg Pro Leu Ala Thr Ala Ala Asp Ser Ala Ala Ser Gly Glu Arg	
450 455 460	
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Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu	
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Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg	
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Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr	
500 505 510	
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Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu	
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Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro	
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Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu	
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Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala	
645 650 655	
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675 680 685	
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Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val	
690 695 700	
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Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala 705 710 715 720	
ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn 725 730 735	2208
gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr 740 745 750	2256
gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala 755 760 765	2304
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly 770 775 780	2352
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn 785 790 795 800	2400
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ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr 820 825 830	2496
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala 835 840 845	2544
agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu 850 855 860	2592
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp 865 870 875 880	2640
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gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu 900 905 910	2736
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala 915 920 925	2784
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945 950 955 960	
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Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile	
965 970 975	
 gag cag tgc gca tcc ggc tgt aca gta cga tgc gcc tgc ggc gcc gtg	2976
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val	
980 985 990	
 ttc cga agc aaa aag gtg gtg gtt tgc tta ccg aca acc ttg tat ccc	3024
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro	
995 1000 1005	
 acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg	3072
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala	
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 gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac	3120
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp	
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Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser	
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 tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga	3216
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg	
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 caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg	3264
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp	
1075 1080 1085	
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Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu	
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 cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac	3360
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn	
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 gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa gga gct ccg	3408
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro	
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 agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgc gcg ctc	3456
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu	
1140 1145 1150	
 aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta	3504
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu	
1155 1160 1165	
 gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt	3552

Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly  
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 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
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 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
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 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
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 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
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 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
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 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
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 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
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 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
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 Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly  
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 Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His  
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 Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp  
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 Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val  
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 Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys  
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 Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala  
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 Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg  
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Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val	Thr	Val	Phe
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Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	Pro	Gln	Thr
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Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	Arg	Val	Leu
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Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	Arg	Ala	Pro
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Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	Gln	Phe	Asn
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Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	Gly	Ala	Pro
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Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	Arg	Ala	Pro
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Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	Phe	Lys	Leu
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Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	Thr	Pro	Ala
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Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala
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Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly
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785				790						795					800
Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu
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 Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala  
 835 840 845  
 Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu  
 850 855 860  
 His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp  
 865 870 875 880  
 Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala  
 885 890 895  
 Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu  
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 Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala  
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 Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr  
 930 935 940  
 Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys  
 945 950 955 960  
 Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile  
 965 970 975  
 Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val  
 980 985 990  
 Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro  
 995 1000 1005  
 Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala  
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 Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp  
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 Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser  
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 Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg  
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 1090 1095 1100  
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 1125 1130 1135  
 Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu  
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 Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu  
 1155 1160 1165  
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<223> Glyc(-)APAO coding sequence; mutation in putative glycosylation sites

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gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg      96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
          20          25          30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct      144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
          35          40          45

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc      192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
          50          55          60

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac      240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
          65          70          75

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg      288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
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ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg      336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
          100          105          110

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc      384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
          115          120          125

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg      432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
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gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc      480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
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cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta      528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
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ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc      576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
          180          185          190

aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta      624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
          195          200          205

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg      672
Ser Arg Leu Phe Glu Arg Phe His Leu Gly Glu Leu Gln Arg Thr

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cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg			768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala			
	245	250	255
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa			816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln			
	260	265	270
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc			864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe			
	275	280	285
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta			912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			
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gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc			960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			
	305	310	315
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt			1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			
	325	330	335
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa			1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			
	340	345	350
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca			1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			
	355	360	365
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca			1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
	370	375	380
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa			1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
	385	390	395
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Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
	405	410	415
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc			1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
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ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg			1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
	435	440	445

cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460	1392
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acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 485 490 495	1488
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gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 515 520 525	1584
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 35 40 45  
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
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 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
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 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly



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Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly
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37

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ccgttcaagt	gtgttcattt	cgttggaacg	gagacgtctt	tagtttggaa	agggtatatg	1860
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 <212> PRT  
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<400> 36

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Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
				85					90					95	
Leu	Lys	Ser	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
			115				120					125			
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
			130			135					140				
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165					170					175		
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
			180					185					190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
	195					200					205				
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
	210					215					220				
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
225					230					235					240
Pro	Tyr	Gly	Asp	Ser	Pro	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
			245						250				255		
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	Tyr	Ser	Leu	Glu
			260					265					270		
Asp	Pro	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe
		275					280					285			
Ala	His	Tyr	Cys	Glu	Lys	Asp	Leu	Asn	Leu	Pro	Ala	Val	Leu	Ser	Val
	290					295					300				
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile
305					310					315				320	
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser
			325						330				335		
Asn	Ile	Val	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys
		340						345					350		

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
 355 360 365  
 Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala  
 370 375 380  
 Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
 385 390 395 400  
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
 405 410 415  
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile  
 420 425 430  
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp  
 435 440 445  
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
 450 455 460  
 Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile  
 465 470 475 480  
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
 485 490 495  
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
 500 505 510  
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
 515 520 525  
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
 530 535 540  
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
 545 550 555 560  
 Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
 565 570 575  
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
 580 585 590  
 Val Ala Ser Leu Val Pro Ala Ala  
 595 600

<210> 37  
 <211> 1929  
 <212> DNA  
 <213> *Exophiala spinifera*

<220>  
 <221> intron  
 <222> (739)...(811)

<221> intron  
 <222> (1134)...(1186)

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 gacgctttgg gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attcgccaat 180  
 ctgcgagctt gccttgctgc agttggagcc tcttcaaagc acgtcaccaa gctcaattac 240  
 tacatcgtcg actacgcccc gagcaaaccc accgcaattg gagatgggct gaagtctacc 300  
 tttgcccttg acaggctccc tcttgacag ctggtgccag taccggcctt ggcttcacct 360  
 gaatacctct ttgaggttga cgccacggcg ctggtgccag gacactcgac cccagacaaac 420  
 gttgcggacg tggtagtggt gggcgctggc ttgagcggct tggagacggc acgcaaagtc 480  
 caggccgccg gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaaagact 540  
 ctgagcgtac aatcgggctc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600  
 aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggaggcgag 660  
 ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720

ccttatgggtg	actccccggt	aagcacaatc	ccactttgtg	atgagacctc	tgtcgagtgt	780
agaatacagt	cactgactcc	acttcgtcca	gctgagcgag	gaggttgcaa	gtgcaattgc	840
ggaactcctc	cccgtatggg	ctcagctgat	cgaagagtat	agccttgaag	accccaaggc	900
gagccctcag	gcgaagcggc	tcgacagtgt	gagcttcgcg	cactactgtg	agaaggacct	960
aaacttgctt	gctgtttctc	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcgggtgtgga	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcc	ccgggtctcag	1080
taatattgtc	tcggacaaga	aagacggcgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
cggtgtcctc	tcaggtaggg	gactcgtttc	ttagtggtca	ttccagggtat	gcagtcgatt	1200
tgccatgcc	tgtcaaagga	acttgttcca	ggctcagtcg	acctcaacac	ccccgtcgt	1260
ggaattgagc	agtccggctc	cggctgtata	gtacgatcgg	cctcggggcgc	cgtgttcgga	1320
agcaaaaagg	tggtggtttc	gttaccgaca	acattgtatc	ccaccttgac	attttccacca	1380
cctcttcccg	ccgagaagca	agcattggcg	gaaaaatcta	tcctcgggta	ctatagcaag	1440
atagtcttcg	tatgggacaa	cccgtgggtg	cgcgaaacaag	gcttctcggg	cgctctccaa	1500
tcgagctgtg	accccatctc	atttgccaga	gataaccaga	tcgaagtcca	tcggcaatgg	1560
tcctttacct	gtttcatggt	cggagaccgg	ggacgggaagt	ggcccccaaca	gtccaaagcag	1620
gtacgacaaa	agtctgtctg	ggaccaactc	cgcgcagcct	acgagaacgc	cgggggccccaa	1680
gtcccagagc	cggccaaagt	gttcgaaatc	gagtggtcca	agcagcagta	tttccaaagga	1740
gtcccgagcg	ccgtctatgg	gctgaacgat	ctcatcaaac	tgggttcggc	gtccagaacg	1800
ccgttcaagt	gtgttcattt	cgttggaacg	gagacgtctt	tagtttggaa	aggggtatatg	1860
gaaggggcca	tacgatcggg	tcaacgaggt	gctgcagaag	ttgtggctag	cctggtgcc	1920
gcagcatag						1929

<210> 38

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 38

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50						55				60				
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85						90					95	
Leu	Lys	Ser	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120					125			
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135						140			
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165						170				175		
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
			180					185					190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
		195					200					205			
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
	210					215					220				
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
225					230					235				240	





<221> misc\_feature  
 <222> (648)...(648)  
 <223> n = A,T,C or G

<400> 39  
 atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc aggggtattct 60  
 cacgtcggcg taggcccaga cggagggagg tatgtgacaa tagctggaca gattggacaa 120  
 gacgcttcgg gcgtgacaga ccctgcctac gagaacacagg ttgcccagc attcgccaat 180  
 ctgcgagctt gccttgctgc agttggagcc acttcaaacg acgtcaccaa gctcaattac 240  
 tacatcgteg actacgcccc gagcaaaactc accgcaattg gagatgggct gaaggctacc 300  
 tttgcccttg acaggtcccc tccttgcaag ctgggtgccag tgtcggcctt gtcttcacct 360  
 gaatacctct ttgaggttga tgccacggcg ctgggtgcggg gacacacgac cccagacaac 420  
 gttgcggagc tggtagtggg gggcgctggc ttgagcgggt tggagacggc acgcaaagtc 480  
 caggccgcgc gtctgtctct cctcgttctt gagggcgatgg atcgtgtagg gggaaagact 540  
 ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600  
 aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatnt ggagggcgag 660  
 ctccagagga cgactggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720  
 ccttatgggt actccttggg aagcacaatc ccactttgtg atgagacctc tgcagagtgt 780  
 agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa gtgcaettgc 840  
 ggaactctc cccgtatggg ctacagctgat cgaagagcat agccttcaag acctcaaggc 900  
 gagccctcag gcgaagcggc tcgacagtgt gagcttcggc cactactgtg agaaggaaat 960  
 aaacttgccg gctgttctcg gcgtagcaaa ccagatcaaa cgcgctctgc tcgggtgtgga 1020  
 agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcc aagggtctcag 1080  
 taatatcttc tgggacaaga aagacggcgg gcagtatatg cgatgcaaaa cagggtcgtg 1140  
 tgggtgtctc tcagggtggg gactcgtttc tcaagtgggtc atttcaggta tgcagtcgat 1200  
 ttgccatgcc atgtcaaaagg aacttgttcc aggtctcagt caccctcaaca ccccgctcgc 1260  
 tgaaattgag cagtcggcat ccggctgtac agtaacgatg gcctcgggcg ccgtgttccg 1320  
 aagcaaaaag gtgggtggtt cgttaccgac aaccttgat cccaccttga cattttcacc 1380  
 acctctcccc gccgagaagc aagcattggc ggaaaattct atcctgggct actatagcaa 1440  
 gatagtcttc gtatgggaca agccgtgggtg gcgcgaacaa ggcttctcgg gcgtctctca 1500  
 atcgagctgt gaccccatct catttgccag agataccagc atcgacgtcg atcgacaatg 1560  
 gtccattacc tgtttcatgg tcggagaccc gggacggaag tggteccaac agtccaagca 1620  
 ggtacgacaa aagtctgtct gggaccaact ccgcgcagcc tacgagaacg ccggggccca 1680  
 agtcccagag ccggccaacg tgctcgaaat cgagtgggtg aagcagcagt atttccaagg 1740  
 agtcccgagc gccgtctatg ggctgaacga tctcatcaca ctgggttcgg cgtcagaac 1800  
 gccgttcaag agtgttcatt tcgttggaaac ggagacgtct ttagtttgga aagggtatat 1860  
 ggaagggggc atacgatcgg gtcaacgagg tctgcagaa gttgtggcta gcctgggtgc 1920  
 agcagcatag 1930

<210> 40  
 <211> 598  
 <212> PRT  
 <213> Exophiala spinifera

<220>  
 <221> VARIANT  
 <222> (216)...(216)  
 <223> Xaa = Any Amino Acid

<400> 40  
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 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
 20 25 30  
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
 35 40 45  
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys

50	55	60
Leu Ala Ala Val Gly	Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65	70	75
Tyr Ile Val Asp Tyr	Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	80
	85	90
Leu Lys Ala Thr Phe	Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	95
	100	105
Pro Val Ser Ala Leu	Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	110
	115	120
Thr Ala Leu Val Pro	Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	125
	130	135
Val Val Gly Ala Gly	Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln	140
145	150	155
Ala Ala Gly Leu Ser	Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly	160
	165	170
Gly Lys Thr Leu Ser	Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn	175
	180	185
Asp Leu Gly Ala Ala	Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser	190
	195	200
Arg Leu Phe Glu Arg	Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr	205
	210	215
Gly Asn Ser Ile His	Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro	220
225	230	235
Tyr Gly Asp Ser Leu	Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu	240
	245	250
Leu Leu Pro Val Trp	Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp	255
	260	265
Leu Lys Ala Ser Pro	Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala	270
	275	280
His Tyr Cys Glu Lys	Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn	285
	290	295
Gln Ile Thr Arg Ala	Leu Leu Gly Val Glu Ala His Glu Ile Ser Met	300
305	310	315
Leu Phe Leu Thr Asp	Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile	320
	325	330
Phe Ser Asp Lys Lys	Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly	335
	340	345
Met Gln Ser Ile Cys	His Ala Met Ser Lys Glu Leu Val Pro Gly Ser	350
	355	360
Val His Leu Asn Thr	Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly	365
	370	375
Cys Thr Val Arg Ser	Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val	380
385	390	395
Val Val Ser Leu Pro	Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro	400
	405	410
Pro Leu Pro Ala Glu	Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly	415
	420	425
Tyr Tyr Ser Lys Ile	Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu	430
	435	440
Gln Gly Phe Ser Gly	Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe	445
	450	455
Ala Arg Asp Thr Ser	Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys	460
465	470	475
Phe Met Val Gly Asp	Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln	480
	485	490
Val Arg Gln Lys Ser	Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn	495
	500	505
Ala Gly Ala Gln Val	Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp	510

515                      520                      525  
 Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu  
 530                      535                      540  
 Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser  
 545                      550                      555                      560  
 Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met  
 565                      570                      575  
 Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala  
 580                      585                      590  
 Ser Leu Val Pro Ala Ala  
 595

<210> 41  
 <211> 1928  
 <212> DNA  
 <213> Rhinocladiella atrovirens

<220>  
 <221> intron  
 <222> (739)...(811)  
 <221> intron  
 <222> (1134)...(1185)

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 gacgttcggc cctgacaga cctgcctac gagaaacagg ttgcccagc attcgccaac 180  
 ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240  
 tacatcgctc actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc 300  
 tttgcccttg acaggctccc tcttgcaacg ctgggtgccg tgcgggccct ggcttcacct 360  
 gaataccctt ttgaggttga tgccacggcg ctgggtccag gacactcaac cccagacaat 420  
 gttgcggaag tggctcgtgtt gggcgctggc ttgagcgggt tggagacggc acgcaaagtc 480  
 caggctgcgg ggctgtcctg cctcgttctt gagcgatgg atcgtgtggg gggaaagact 540  
 ctgagcgtac aatcgggtcc cggcaggacg gctatcaatg acctcggcgc tgcgtggatc 600  
 aatgacagca accaaaagcga agtattcaaa ttatttgaaa gatttcattt ggaggggcag 660  
 ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720  
 ccttatgggt attccctggg aagcacaatt ccatcttggt atgagacctc tgcgtgtgt 780  
 agaatacagt cgtgactcc acatcgctca gctgagcgag gaggttgcaa gtgcactcgc 840  
 ggaactcctt ccgcctgggt ctacagctgat cgaagagcat agtcttgaag accccaagc 900  
 gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960  
 aagcttgctt gctgttctcg gctgtggcaa ccagatcaca cgcgctctgc tgggtgtgga 1020  
 agcccacgag atcagcatgc tttttctcac cgaactacat aagagtgcga ccggtctcag 1080  
 taatattgtc tcggataaga aagacgggtg gcagtatatg cgatgcaaaa cagggtgcgtg 1140  
 tgggtgttct tcagtgggag actcgtttct tagtggctcat tccaggtatg cagtcgcttt 1200  
 gccatgccat gtcaaaaggaa cttgttccag gctcagtga cctcaacacc ccgctgcgcg 1260  
 aaattgagca gtcggcatcc ggctgtacag taagatcggc ctcgggcggc gtgttcggaa 1320  
 gtaaaaagggt ggtgggttctg ttaccgacaa ccttggtatcc cacttgata ttttcaccac 1380  
 ctcttccgcg cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagcaaga 1440  
 tagtcttcgt atgggacaag ccgtgggtggc gogaacaagg cttctcgggc gtccctccat 1500  
 cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcgat cggcaatggt 1560  
 ccattacctg tttcatggtc ggagaccggc gacggaagtg gtcccaacag tccaagcagg 1620  
 tacgacagaa gtctgtctgg aaccaactcc gcgcagccta cgagaacgcc ggggcccagg 1680  
 tcccagagcc ggccaagctg ctcgagatcg agtggctgaa gcagcagtat ttccaaggag 1740  
 cgcgcagcgt cgtctatggg ctgaactgtc tcaaacactt ggggttcggcg ctccagaacgc 1800  
 cgttcaagggt gtttcaatttc gttggaacgg agaagttctt ggtttggaaa gggtatattg 1860  
 aaggggcat acgatcgggt cagcgaggcg ctgcagaagt tgtggctagc ctgggtgcag 1920  
 cagcatag 1928

<210> 42  
 <211> 598  
 <212> PRT  
 <213> Rhinocladiella atrovirens

<400> 42  
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 20 25 30  
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro  
 35 40 45  
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
 50 55 60  
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr  
 65 70 75 80  
 Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
 85 90 95  
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
 100 105 110  
 Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala  
 115 120 125  
 Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
 130 135 140  
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
 145 150 155 160  
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
 165 170 175  
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile  
 180 185 190  
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
 195 200 205  
 Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly  
 210 215 220  
 Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr  
 225 230 235 240  
 Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu  
 245 250 255  
 Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro  
 260 265 270  
 Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His  
 275 280 285  
 Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn  
 290 295 300  
 Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met  
 305 310 315 320  
 Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile  
 325 330 335  
 Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly  
 340 345 350  
 Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser  
 355 360 365  
 Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly  
 370 375 380  
 Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val  
 385 390 395 400  
 Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro

				405						410					415				
Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Lys	Ser	Ile	Leu	Gly				
			420					425					430						
Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu				
		435					440					445							
Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe				
	450					455					460								
Ala	Arg	Asp	Thr	Ser	Ile	Glu	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys				
465					470					475					480				
Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln				
			485					490						495					
Val	Arg	Gln	Lys	Ser	Val	Trp	Asn	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn				
			500					505					510						
Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp				
		515					520					525							
Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Val	Val	Tyr	Gly	Leu				
	530					535					540								
Asn	Cys	Leu	Asn	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Gly				
545					550					555					560				
Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met				
			565					570						575					
Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala				
			580					585					590						
Ser	Leu	Val	Pro	Ala	Ala														
		595																	

<210> 43  
 <211> 1928  
 <212> DNA  
 <213> *Rhinocycladiella atrovirens*

<220>  
 <221> intron  
 <222> (739)...(811)  
  
 <221> intron  
 <222> (1134)...(1186)

<400> 43																			
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gacgcttcgg	ccgtgacaga	ccctgcctac	gagaaacagg	ttgccc aagc	atcgccaaac														180
ctgcgagctt	gtcttgctgc	agttggagcc	acttcaaaacg	acattaccaa	gtcgaattac														240
tacatcgctg	actacaaccc	gagcaaacctc	accgcaattg	gagatgggct	gaaggctacc														300
tttgcccttg	acaggctccc	tccttgcaag	ctgggtgccag	tgcgggccct	ggcttcacct														360
gaataacctct	ttgaggttga	tgccacggcg	ctgggtccag	gacactcaac	cccagacaat														420
gttgcggaag	tggctgtgtg	ggcgctggc	ttgagcggtt	tggagacggc	acgcaagctc														480
caggctgcag	ggctgtccctg	cctcgttctt	gaggcgatgg	atcgtgtggg	gggaaagact														540
ctgagcgtac	aatcggtgtc	cggcaggacg	actatcaatg	acctcggcgc	tgcgtggatc														600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag														660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct														720
ccttatgggtg	attccctggt	aagcacaatt	ccatcttggtg	atgagacctc	tgtcgtgtgt														780
agaatacagt	cgctgactcc	acatcgctcca	gctgagcgag	gaggttgcaa	gtgcactcgc														840
ggaactcctt	cccgcctggt	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc														900
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct														960
aaacttgctt	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tgggtgtgga														1020
agcccacgag	atcagcatgt	tttttctcac	cgactacatc	aagagtgcc	ccggtctcag														1080
taatattgtc	tcggataaga	aagacgggtg	gcagttatatg	cgatgcaaaa	caggtgcgtg														1140

tggtgtttctc	tcagtgggag	actcgtttct	tagtgggtcat	tcaggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaggaa	cttgttccag	gtcagtgca	cctcaacacc	cccgtcgcgc	1260
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcggc	ctcggggcgc	gtgttccgaa	1320
gtaaaaaggt	ggtggtttcg	ttaccgacaa	ccttgatcc	caccttgata	ttttcaccac	1380
ctcttccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ccgtggtggc	gcgaacaagg	cttctcgggc	gtctctcaat	1500
cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggcaatggt	1560
ccattacctg	tttcatggtc	ggagaccgg	gacggaagt	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcgcagccta	cgagaacgcc	ggggcccaag	1680
tcccagagcc	ggccaacgtg	ctcgagatcg	agtgggtcgaa	gcagcagtat	ttccaaggag	1740
cgcgcagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tggtcatttc	ggttgaacgg	agacgtcttt	gggttggaaa	gggtatatgg	1860
aaggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtggctagc	ctggtgccag	1920
cagcatag						1928

<210> 44

<211> 591

<212> PRT

<213> *Rhinocladiella atrovirens*

<400> 44

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Leu	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	Tyr	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr
65					70				75					80	
Tyr	Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85					90						95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120					125			
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135					140				
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165					170					175		
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Gly	Arg	Thr	Thr	Ile	Asn
		180					185					190			
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Lys
	195					200					205				
Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly
	210				215						220				
Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr
225				230					235					240	
Gly	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu
			245					250					255		
Pro	Ala	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Glu	Asp	Pro	Lys	Ala
		260					265					270			
Ser	Pro	Gln	Ala	Lys	Gln	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys
	275					280					285				
Glu	Lys	Leu	Asn	Leu	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg

290		295		300											
Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Phe	Phe	Leu	Thr
305					310					315					320
Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Val	Ser	Asp	Lys
			325						330					335	
Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Leu
		340						345					350		
Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn
	355					360						365			
Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg
	370					375					380				
Ser	Ala	Ser	Gly	Gly	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Leu	Pro	Thr
385					390					395					400
Leu	Tyr	Pro	Thr	Leu	Ile	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
			405						410					415	
Ala	Leu	Ala	Glu	Lys	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
		420						425					430		
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
	435					440					445				
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Glu
	450					455					460				
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
465					470					475					480
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
			485						490					495	
Asn	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
		500						505					510		
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
	515						520					525			
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Cys	Leu	Asn	Thr	Leu	Gly
	530					535					540				
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Gly	Val	His	Phe	Val	Gly	Thr	Glu
545					550					555					560
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
			565						570					575	
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
		580						585					590		

<210> 45  
 <211> 1928  
 <212> DNA  
 <213> *Rhinocycladiella atrovirens*

<220>  
 <221> intron  
 <222> (739)...(811)

<221> intron  
 <222> (1134)...(1185)

<400> 45	
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cacgtcggcg taggcacaaa cggagggagg tatgtgacaa tagctggaca gattggacaa	120
gacgtttcgg ccgtgacaga cctgcctac gagaaacagg ttgcccaagc attcgccaac	180
ctgcgagctt gtcttctctgc agttggagcc acttcaaacg acattaccaa gctcaattac	240
tacatcgtcg actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc	300
tttgcccttg acaggtctcc tctttgcaag ctgggtgcag tgccggccct ggtttcacct	360
gaatacctct ttgaggttga tgctacggcg ctgggttcag gacactcaac ccagacaa	420

gttgcggaacg	tggtcgtggt	gggcgctggc	ttgagcggtt	tggagacggc	acgcaaagtc	480
caggctgccg	ggctgtcctg	cctcgttcct	gaggcgatgg	atcgtgtggg	gggaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggacg	actatcaatg	acctcggcgc	tgcgtggatc	600
aatgacagca	accaaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatgggt	attccctggt	aggcacaatt	ccatcttggt	atgagacctc	tgtcgtgtgt	780
agaatacagt	cgctgactcc	acatcgctcc	gctgagcgag	gaggttgcaa	gtgcactcgc	840
ggaactcctt	cccgcattgt	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
aaacttgccct	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgccca	ccggtctcag	1080
taatattgtc	tcggataaga	aagaacggtg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
tggtgttctc	tcagtgggag	actcgtttct	tagtggtcat	tcaggtatg	cagtgcgttt	1200
gccatgccat	gtcaaaggaa	cttgttccag	gctcagtcca	cctcaacacc	cccgctcgccg	1260
aaattgagca	gtcggcatcc	ggctgtacag	taagatcggc	ctcgggcggc	gtgttccgaa	1320
gtaaaaaggt	ggtggtttcg	ttaccgacaa	ccttggtatcc	caccttgata	ttttcaccac	1380
ctcttcccg	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaa	ctgtggtggc	gcgaacaagg	cttctcgggc	gtctctcaat	1500
cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggaatggt	1560
ccattacctg	tttcatggtc	ggagaccggg	gaagggaagt	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcgcagccta	cgagaacgcc	ggggcccaag	1680
tcccagagcc	ggccaacgtg	ctcgagatgc	agtggtcgaa	gcagcagtat	ttccaaggag	1740
cgccgagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tggttcatttc	gttggaacgg	agaagctctt	ggtttgaaa	gggtatatgg	1860
aaggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtgcctagc	ctggtgccag	1920
cagcatag						1928

<210> 46

<211> 591

<212> PRT

<213> *Rhinocycladiella atrovirens*

<400> 46

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Ala	Ser	Pro	Ala
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Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Val	Thr
			20					25					30		
Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro	Ala
			35				40					45			
Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	Leu
			50				55				60				
Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr	Tyr
65					70				75					80	
Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	Leu
			85					90					95		
Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	Pro
			100					105					110		
Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	Thr
			115				120					125			
Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	Val
			130				135					140			
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
145					150				155					160	
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
			165					170					175		
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
			180					185					190		
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Phe







Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser
			485					490						495	
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr
			500					505					510		
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile
	515						520				525				
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr
	530					535					540				
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe
545					550					555					560
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly
			565					570						575	
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val
			580					585					590		
Val	Ala	Ser	Leu	Val	Pro	Ala	Ala								
		595				600									

<210> 48  
 <211> 1392  
 <212> DNA  
 <213> Unknown

<220>  
 <221> CDS  
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteine 461

<400> 43																
aaa	gac	aac	gtt	gcg	gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggc	48
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	
1				5					10				15			
ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggc	ctg	tcc	tgc	ctc	gtt	96
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	
			20					25					30			
ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tgc	144
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	
			35				40					45				
ggc	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	192
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	
	50					55				60						
gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	240
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	
	65				70				75				80			
gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	288
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	
			85					90					95			
gac	ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	336
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
			100					105					110			
gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	384

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *	
450 455 460	

<210> 49  
 <211> 463  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Cys (-) APAO; removal of cysteine 461

<400> 49

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	

145		150		155		160									
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
		165				170								175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
		180						185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
		195					200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
	210					215				220					
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235				240	
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245					250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260						265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
	275						280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
290					295						300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315				320	
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
			325					330					335		
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
		340						345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
	355						360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
370					375					380					
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385			390						395					400	
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
		405						410					415		
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
		420						425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
	435					440						445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
450					455					460					

<210> 50  
 <211> 1392  
 <212> DNA  
 <213> Unknown

<220>  
 <221> CDS  
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 50	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	

20	25	30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 35 40 45			144
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50 55 60			192
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 65 70 75 80			240
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85 90 95			288
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 100 105 110			336
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125			384
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130 135 140			432
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160			480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175			528
ggc gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190			576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205			624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210 215 220			672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240			720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255			768

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tgc tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270	816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tgc ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tgc agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350	1056
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385 390 395 400	1200
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405 410 415	1248
tgc gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420 425 430	1296
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgc ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435 440 445	1344
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala * 450 455 460	1392

<210> 51  
 <211> 463  
 <212> PRT  
 <213> Unknown



<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Gly	Leu	Ser	Cys	Leu	Val	
			20					25				30			
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
		35					40				45				
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn
50						55				60					
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
65					70					75				80	
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
				85				90					95		
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu
			100					105					110		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
130						135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155				160	
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
			165					170						175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
		195					200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Ser	His	Ala
210						215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230						235				240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
			245						250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260						265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
		275					280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
		290				295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315				320	
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
			325						330					335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
		340						345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
		355					360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
		370				375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385					390						395				400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
			405						410					415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
		420						425						430	

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445  
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 52  
<211> 1392  
<212> DNA  
<213> Unknown

<220>  
<221> CDS  
<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 169, 359, and  
461

<400> 52  
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48  
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15  
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt 96  
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val  
20 25 30  
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144  
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45  
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192  
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60  
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240  
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80  
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288  
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95  
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336  
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110  
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg 384  
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125  
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag 432  
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140  
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac 480  
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160

ttg cct gct gtt etc ggc gta gca aac cag atc aca cgc gct ctg etc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggc gtg gaa gcc cac gag atc agc atg ctt ttt etc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt etc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac etc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc etc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa etc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg etc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	

385	390	395	400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt				1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag				1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt				1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	435	440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag				1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *	450	455	460	

<210> 53  
 <211> 463  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Cys (-) APAO; removal of cysteines 169, 359, and  
 461

<400> 53

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly				
1 5 10 15				
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val				
20 25 30				
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser				
35 40 45				
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn				
50 55 60				
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu				
65 70 75 80				
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln				
85 90 95				
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu				
100 105 110				
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu				
115 120 125				
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys				
130 135 140				
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn				
145 150 155 160				
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu				
165 170 175				
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile				
180 185 190				
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly				
195 200 205				
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala				
210 215 220				
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val				

